Nucleotide Sequence of Rhesus Monkey BRS-3

```
   1 ATGGCTCAAA GGCAGCCTCA CTCACCTAAT CAGACTTTAA TTTCAATCAC
  51 AAATGACACA GAATCAAGCT CTGTGGTTTC TAACGATAAC ACAAATAAAG
 101 GACGGAGCGG GGACAACTCT CCAGGAATAG AAGCATTGTG TGCCATCTAT
 151 ATTACTTATG CTGTGATCAT TTCAGTGGGC ATCCTTGGAA ATGCTATTCT
 201 CATCAAAGTC TTTTTCAAGA CCAAATCCAT GCAAACAGTT CCAAATATTT
 251 TCATCACCAG CCTGGCTTTT GGAGATCTTT TACTTCTGCT AACTTGTGTG
 301 CCAGTGGATG CAACCCACTA CCTTGCAGAA GGATGGCTGT TCGGAAGAAT
 351 TGGTTGTAAG GTGCTCTCTT TCATCCGGCT CACTTCTGTT GGTGTGTCAG
 401 TGTTCACGTT AACAATTCTC AGCGCTGACA GATACAAGGC AGTTGTGAAG
 451 CCACTTGAGC GACAGCCCTC CAATGCCATC CTGAAGACTT GTATAAAAGC
 501 TGGCTGCGTC TGGATCGTGT CTATGATATT TGCTCTACCT GAGGCTATAT
 551 TTTCAAATGT ATATTCTTTT CGAGATCCCA ACAAAAATGT GACATTTGAA
 601 TCGTGTACCT CTTATCCTGT CTCTAAGAAG CTCTTGCAAG AAATACATTC
 651 TCTGCTGTGC TTCTTAGTGT TCTACATTAT TCCACTCTCT ATTATCTCTG
 701 TCTATTATTC TTTGATTGCT AGGACCCTTT ATAAAAGCAC CCTGAACATA
 751 CCTACTGAGG AACAAGGCCA TGCCCGTAAG CAGATTGAAT CCCGGAAGAG
 801 AATTGCCAGA ACGGTATTGG TGTTGGTGGC TCTGTTTGCC CTCTGCTGGT
 851 TGCCAAATCA CCTCCTGTAC CTCTACCATT CATTCACTTC TCAAACCTAT
 901 GTAGACCCCT CTGCCATGCA TTTCATTTTC ACCATTTTCT CTCGGGTTCT
 951 GGCTTTCAGC AATTCTTGCG TAAACCCCTT TGCTCTCTAC TGGCTGAGCA
1001 AAACCTTCCA GAAGCATTTT AAAGCTCAGT TGTTCTGTTG CAAGGCAGAG
1051 CAGCCTGAGC CTCCTGTTGC TGACACCTCT CTTACCACCC TGGCTGTGAT
1101 GGGAAGGGTC CCGGGCACTG GGAACATGCA GATGTCTGAA ATTAGTGTGA
1151 CCTCGTTCCC TGGGTGTAGT GTGAAGCAGG CAGAGGATAG AGTCTAG
```

FIG.1 (SEQ ID NO:1)

Amino Acid Sequence of Rhesus Monkey BRS-3 Protein

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   1 MAQRQPHSPN QTLISITNDT ESSSVVSNDN TNKGRSGDNS PGIEALCAIY
  51 ITYAVIISVG ILGNAILIKV FFKTKSMQTV PNIFITSLAF GDLLLLLTCV
 101 PVDATHYLAE GWLFGRIGCK VLSFIRLTSV GVSVFTLTIL SADRYKAVVK
 151 PLERQPSNAI LKTCIKAGCV WIVSMIFALP EAIFSNVYSF RDPNKNVTFE
 201 SCTSYPVSKK LLQEIHSLLC FLVFYIIPLS IISVYYSLIA RTLYKSTLNI
 251 PTEEQGHARK QIESRKRIAR TVLVLVALFA LCWLPNHLLY LYHSFTSQTY
 301 VDPSAMHFIF TIFSRVLAFS NSCVNPFALY WLSKTFQKHF KAQLFCCKAE
 351 QPEPPVADTS LTTLAVMGRV PGTGNMQMSE ISVTSFPGCS VKQAEDRV
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(SEQ ID NO:2)

FIG.2

ALIGNMENT OF BRS-3 NUCLEOTIDE SEQUENCES

```
            (1)  1        10        20        30        40          52
hBRS3       (1)  ATGGCTCAAAGGCAGCCTCACTCACCTAATCAGACTTTAATTTCAATCACAA
ratBRS3     (1)  ATGTCTCAAAGGCAGCCTCAGTCACCTAATCAGACTTTAATTTCCATTACAA
rhBRS3      (1)  ATGGCTCAAAGGCAGCCTCACTCACCTAATCAGACTTTAATTTCAATCACAA
Consensus   (1)  ATGGCTCAAAGGCAGCCTCACTCACCTAATCAGACTTTAATTTCAATCACAA

           (53)  53      60        70        80        90          104
hBRS3      (53)  ATGACACAGAATCATCAAGCTCTGTGGTTTCTAACGATAACACAAATAAAGG
ratBRS3    (53)  ATGACACAGAAACATCAAGCTCTGCCGTCTCCAACGATACTACACCTAAAGG
rhBRS3     (53)  ATGACACAGA---ATCAAGCTCTGTGGTTTCTAACGATAACACAAATAAAGG
Consensus  (53)  ATGACACAGAA CATCAAGCTCTGTGGTTTCTAACGATAACACAAATAAAGG

          (105)  105  110       120       130       140         156
hBRS3     (105)  ATGGAGCGGGGACAACTCTCCAGGAATAGAAGCATTGTGTGCCATCTATATT
ratBRS3   (105)  ATGGACCGGAGACAACTCTCCAGGAATAGAAGCACTGTGTGCCATCTATATC
rhBRS3    (102)  ACGGAGCGGGGACAACTCTCCAGGAATAGAAGCATTGTGTGCCATCTATATT
Consensus (105)  ATGGAGCGGGGACAACTCTCCAGGAATAGAAGCATTGTGTGCCATCTATATT

          (157)  157          170       180       190               208
hBRS3     (157)  ACTTATGCTGTGATCATTTCAGTGGGCATCCTTGGAAATGCTATTCTCATCA
ratBRS3   (157)  ACTTATGCTGTGATCATTTCAGTGGGCATCCTCGGAAATGCTATCCTCATCA
rhBRS3    (154)  ACTTATGCTGTGATCATTTCAGTGGGCATCCTTGGAAATGCTATTCTCATCA
Consensus (157)  ACTTATGCTGTGATCATTTCAGTGGGCATCCTTGGAAATGCTATTCTCATCA

          (209)  209       220       230       240       250       260
hBRS3     (209)  AAGTCTTTTTCAAGACCAAATCCATGCAAACAGTTCCAAATATTTTCATCAC
ratBRS3   (209)  AAGTCTTTTTCAAGACTAAATCCATGCAAACAGTTCCAAATATTTTCATCAC
rhBRS3    (206)  AAGTCTTTTTCAAGACCAAATCCATGCAAACAGTTCCAAATATTTTCATCAC
Consensus (209)  AAGTCTTTTTCAAGACCAAATCCATGCAAACAGTTCCAAATATTTTCATCAC
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FIG.3A

```
          (261) 261      270      280      290      300         312
hBRS3     (261) CAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTTGTGTGCCAGTGGAT
ratBRS3   (261) CAGCCTGGCTTTTGGAGATCTGTTACTCCTGCTGACTTGTGTGCCAGTGGAT
rhBRS3    (258) CAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTTGTGTGCCAGTGGAT
Consensus (261) CAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTTGTGTGCCAGTGGAT

          (313) 313    320       330       340       350        364
hBRS3     (313) GCAACTCACTACCTTGCAGAAGGATGGCTGTTCGGAAGAATTGGTTGTAAGG
ratBRS3   (313) GCAACCCACTACCTGGCAGAGGGATGGCTGTTTGGAAAGGTCGGTTGTAAAG
rhBRS3    (310) GCAACCCACTACCTTGCAGAAGGATGGCTGTTCGGAAGAATTGGTTGTAAGG
Consensus (313) GCAACCCACTACCTTGCAGAAGGATGGCTGTTCGGAAGAATTGGTTGTAAGG

          (365) 365  370       380       390       400             416
hBRS3     (365) TGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCAGTGTTCACATTAAC
ratBRS3   (365) TGCTTTCCTTCATCCGGCTCACTTCTGTCGGTGTATCAGTGTTCACGCTGAC
rhBRS3    (362) TGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCAGTGTTCACGTTAAC
Consensus (365) TGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCAGTGTTCACGTTAAC

          (417) 417         430       440       450               468
hBRS3     (417) AATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAG
ratBRS3   (417) AATTCTCAGCGCTGACAGATACAAAGCAGTCGTGAAGCCACTTGAACGACAG
rhBRS3    (414) AATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAG
Consensus (417) AATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAG

          (469) 469        480       490       500       510       520
hBRS3     (469) CCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCG
ratBRS3   (469) CCCTCCAATGCCATTCTGAAGACCTGTGCCAAAGCTGGTGGCATCTGGATCA
rhBRS3    (466) CCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCG
Consensus (469) CCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCG
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FIG.3B

```
                (521) 521       530       540       550       560       572
hBRS3           (521) TGTCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTT
ratBRS3         (521) TGGCTATGATATTTGCTCTGCCAGAGGCTATATTCTCAAATGTATACACTTT
rhBRS3          (518) TGTCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATATTCTTT
Consensus       (521) TGTCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTT

                (573) 573     580       590       600       610       624
hBRS3           (573) TCGAGATCCCAATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTC
ratBRS3         (573) CCAAGATCCTAACAGAAACGTAACATTTGAATCCTGTAACTCCTACCCTATC
rhBRS3          (570) TCGAGATCCCAACAAAAATGTGACATTTGAATCGTGTACCTCTTATCCTGTC
Consensus       (573) TCGAGATCCCAACAAAAATGTGACATTTGAATCATGTACCTCTTATCCTGTC

                (625) 625     630     640       650       660         676
hBRS3           (625) TCTAAGAAGCTCTTGCAAGAAATACATTCTCTGCTGTGCTTCTTAGTGTTCT
ratBRS3         (625) TCTGAGAGGCTTTTGCAGGAAATACATTCTCTGTTGTGTTTCTTGGTGTTCT
rhBRS3          (622) TCTAAGAAGCTCTTGCAAGAAATACATTCTCTGCTGTGCTTCTTAGTGTTCT
Consensus       (625) TCTAAGAAGCTCTTGCAAGAAATACATTCTCTGCTGTGCTTCTTAGTGTTCT

                (677) 677         690       700       710         728
hBRS3           (677) ACATTATTCCACTCTCTATTATCTCTGTCTACTATTCCTTGATTGCAGGAC
ratBRS3         (677) ACATTATCCCGCTCTCGATTATCTCTGTCTATTATTCTTTGATTGCCAGGAC
rhBRS3          (674) ACATTATTCCACTCTCTATTATCTCTGTCTATTATTCTTTGATTGCTAGGAC
Consensus       (677) ACATTATTCCACTCTCTATTATCTCTGTCTATTATTCTTTGATTGCTAGGAC

                (729) 729       740       750       760       770       780
hBRS3           (729) CCTTTACAAAAGCACCCTGAACATACCTACTGAGGAACAAAGCCATGCCCGT
ratBRS3         (729) TCTTTACAAAAGCACCTTGAACATACCGACTGAGGAACAAAGCCATGCCCGA
rhBRS3          (726) CCTTTATAAAAGCACCCTGAACATACCTACTGAGGAACAAGGCCATGCCCGT
Consensus       (729) CCTTTACAAAAGCACCCTGAACATACCTACTGAGGAACAAAGCCATGCCCGT
```

FIG.3C

```
           (781) 781      790       800       810       820      832
     hBRS3 (781) AAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTTGGTGG
   ratBRS3 (781) AAGCAGATTGAATCCCGGAAGAGAATTGCCAAAACGGTACTGGTGCTGGTGG
    rhBRS3 (778) AAGCAGATTGAATCCCGGAAGAGAATTGCCAGAACGGTATTGGTGTTGGTGG
 Consensus (781) AAGCAGATTGAATCCCGGAAGAGAATTGCCAGAACGGTATTGGTGTTGGTGG

           (833) 833    840       850       860       870            884
     hBRS3 (833) CTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCTCCTGTACCTCTACCATTC
   ratBRS3 (833) CTCTGTTCGCACTCTGCTGGTTGCCGAATCACCTCCTGTATCTCTATCACTC
    rhBRS3 (830) CTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCTCCTGTACCTCTACCATTC
 Consensus (833) CTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCTCCTGTACCTCTACCATTC

           (885) 885  890       900       910       920            936
     hBRS3 (885) ATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTCATTTTCACC
   ratBRS3 (885) ATTCACTTATGAAAGCTACGCAGAGCCTTCTGATGTCCCTTTCGTTGTCACC
    rhBRS3 (882) ATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTCATTTTCACC
 Consensus (885) ATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTCATTTTCACC

           (937) 937          950       960       970                988
     hBRS3 (937) ATTTTCTCTCGGGTTTTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTC
   ratBRS3 (937) ATTTTCTCTCGGGTGCTGGCTTTCAGTAATTCCTGCGTGAACCCCTTTGCTC
    rhBRS3 (934) ATTTTCTCTCGGGTTCTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTC
 Consensus (937) ATTTTCTCTCGGGTTCTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTC

           (989) 989        1000      1010      1020      1030     1040
     hBRS3 (989) TCTACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTG
   ratBRS3 (989) TGTATTGGCTGAGCAAGACCTTCCAGAAGCATTTTAAGGCTCAGCTCTGCTG
    rhBRS3 (986) TCTACTGGCTGAGCAAAACCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTG
 Consensus (989) TCTACTGGCTGAGCAAAACCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTG
```

FIG.3D

```
          (1041) 1041      1050      1060      1070      1080      1092
hBRS3     (1041) TTGCAAGGCGGAGCGGCCTGAGCCTCCTGTTGCTGACACCTCTCTTACCACC
ratBRS3   (1041) CTTCAAGGCAGAGCAGCCTGAACCTCCTCTTGGTGACACCCCCCTTAACAAC
rhBRS3    (1038) TTGCAAGGCAGAGCAGCCTGAGCCTCCTGTTGCTGACACCTCTCTTACCACC
Consensus (1041) TTGCAAGGCAGAGCAGCCTGAGCCTCCTGTTGCTGACACCTCTCTTACCACC

          (1093) 1093 1100      1110      1120      1130      1144
hBRS3     (1093) CTGGCTGTGATGGGAACGGTCCCGGGCACTGGGAGCATACAGATGTCTGAAA
ratBRS3   (1093) CTCACTGTGATGGGGCGGGTTCCAGCTACTGGGAGTGCACACGTCTCTGAAA
rhBRS3    (1090) CTGGCTGTGATGGGAAGGGTCCCGGGCACTGGGAACATGCAGATGTCTGAAA
          (1093) CTGGCTGTGATGGGAAGGGTCCCGGGCACTGGGAGCATACAGATGTCTGAAA

          (1145) 1145 1150      1160      1170      1180      1196
hBRS3     (1145) TTAGTGTGACCTCGTTCACTGGGTGTAGTGTGAAGCAGGCAGAGGACAGATT
ratBRS3   (1145) TTAGCGTGACCCTGTTTAGTGGCAGTACTGCCAAGAAAGGAGAGGACAAAGT
rhBRS3    (1142) TTAGTGTGACCTCGTTCCCTGGGTGTAGTGTGAAGCAGGCAGAGGATAGAGT
Consensus (1145) TTAGTGTGACCTCGTTCACTGGGTGTAGTGTGAAGCAGGCAGAGGACAGAGT

          (1197) 1197 2000
hBRS3     (1197) CTAG (SEQ. ID NO: 17)
ratBRS3   (1197) TTAG (SEQ. ID NO: 18)
rhBRS3    (1194) CTAG (SEQ. ID NO: 1)
Consensus (1197) CTAG (SEQ. ID NO: 19)
```

FIG.3E

ALIGNMENT OF BRS-3 AMINO ACID SEQUENCES

```
          (1)   1        10        20        30        40          53
    hBRS3 (1)   MAQRQPHSPNQTLISITNDTESSSSVVSNDNTNKGWSGDNSPGIEALCAIYIT
  ratBRS3 (1)   MSQRQPQSPNQTLISITNDTETSSSAVSNDTTPKGWTGDNSPGIEALCAIYIT
   rhBRS3 (1)   MAQRQPHSPNQTLISITNDTE-SSSVVSNDNTNKGRSGDNSPGIEALCAIYIT
Consensus (1)   MAQRQPHSPNQTLISITNDTESSSSVVSNDNTNKGWSGDNSPGIEALCAIYIT

          (54)  54   60        70        80        90              106
    hBRS3 (54)  YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT
  ratBRS3 (54)  YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT
   rhBRS3 (53)  YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT
Consensus (54)  YAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLLLLTCVPVDAT

          (107) 107          120       130       140                 159
    hBRS3 (107) HYLAEGWLFGRIGCKVLSFIRLTSVGVSVFTLTILSADRYKAVVKPLERQPSN
  ratBRS3 (107) HYLAEGWLFGKVGCKVLSFIRLTSVGVSVFTLTILSADRYKAVVKPLERQPSN
   rhBRS3 (106) HYLAEGWLFGRIGCKVLSFIRLTSVGVSVFTLTILSADRYKAVVKPLERQPSN
Consensus (107) HYLAEGWLFGRIGCKVLSFIRLTSVGVSVFTLTILSADRYKAVVKPLERQPSN

          (160) 160       170       180       190       200          212
    hBRS3 (160) AILKTCVKAGCVWIVSMIFALPEAIFSNVYTFRDPNKNMTFESCTSYPVSKKL
  ratBRS3 (160) AILKTCAKAGGIWIMAMIFALPEAIFSNVYTFQDPNRNVTFESCNSYPISERL
   rhBRS3 (159) AILKTCIKAGCVWIVSMIFALPEAIFSNVYSFRDPNKNVTFESCTSYPVSKKL
Consensus (160) AILKTCIKAGCVWIVSMIFALPEAIFSNVYTFRDPNKNVTFESCTSYPVSKKL

          (213) 213    220       230       240       250             265
    hBRS3 (213) LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES
  ratBRS3 (213) LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES
   rhBRS3 (212) LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQGHARKQIES
Consensus (213) LQEIHSLLCFLVFYIIPLSIISVYYSLIARTLYKSTLNIPTEEQSHARKQIES
```

FIG.4A

	(266)	266 280 290 300 318
hBRS3	(266)	RKRIARTVLVLVALFALCWLPNHLLYLYHSFTSQTYVDPSAMHFIFTIFSRVL
ratBRS3	(266)	RKRIAKTVLVLVALFALCWLPNHLLYLYHSFTYESYAEPSDVPFVVTIFSRVL
rhBRS3	(265)	RKRIARTVLVLVALFALCWLPNHLLYLYHSFTSQTYVDPSAMHFIFTIFSRVL
Consensus	(266)	RKRIARTVLVLVALFALCWLPNHLLYLYHSFTSQTYVDPSAMHFIFTIFSRVL

	(319)	319 330 340 350 360 371
hBRS3	(319)	AFSNSCVNPFALYWLSKSFQKHFKAQLFCCKAERPEPPVADTSLTTLAVMGTV
ratBRS3	(319)	AFSNSCVNPFALYWLSKTFQKHFKAQLCCFKAEQPEPPLGDTPLNNLTVMGRV
rhBRS3	(318)	AFSNSCVNPFALYWLSKTFQKHFKAQLFCCKAEQPEPPVADTSLTTLAVMGRV
Consensus	(319)	AFSNSCVNPFALYWLSKTFQKHFKAQLFCCKAEQPEPPVADTSLTTLAVMGRV

	(372)	372 380 399	
hBRS3	(372)	PGTGSIQMSEISVTSFTGCSVKQAEDRF	(SEQ. ID NO:20)
ratBRS3	(372)	PATGSAHVSEISVTLFSGSTAKKGEDKV	(SEQ. ID NO:21)
rhBRS3	(371)	PGTGNMQMSEISVTSFPGCSVKQAEDRV	(SEQ. ID NO:2)
Consensus	(372)	PGTGSIQMSEISVTSFSGCSVKQAEDRV	(SEQ. ID NO:22)

FIG.4B